

10/576030

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SEQUENCE LISTING

<110> Hokko CHEMICAL INDUSTRY CO., LTD.
<120> METHOD FOR PRODUCING SCYLLO-INOSITOL
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aaa acc ttc cat gcg ccc ctg att gcg ggc acg ccc ggg cag gaa ctg 96
Lys Thr Phe His Ala Pro Leu Ile Ala Gly Thr Pro Gly Gin Glu Leu
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gcg gta atc tcc agc agt gat gaa aca aaa gta aaa gcc gac tgg cca 144
Ala Val Ile Ser Ser Asp Glu Thr Lys Val Lys Ala Asp Trp Pro
35 40 45
acg gtt acg gtt gtc tct gag ccg aag cat ctg ttt aac gat ccc aac 192
Thr Val Thr Val Val Ser Glu Pro Lys His Leu Phe Asn Asp Pro Asn
50 55 60

ata gac ctg att gtc att cct aca ccc aac gat acc cat ttc cog tta Ile Asp Leu Ile Val Ile Pro Thr Pro Asn Asp Thr His Phe Pro Leu 65 70 75 80	240
gcc aaa gcg gcg ctt gag gcg ggt aaa cat gtg gtc gtt gat aaa ccc Ala Lys Ala Ala Leu Glu Ala Gly Lys His Val Val Val Asp Lys Pro 85 90 95	288
ttt acc gtg aca ctg tca caa gcg cga gag ctg gat gcg ctg gca aaa Phe Thr Val Thr Leu Ser Gln Ala Arg Glu Leu Asp Ala Leu Ala Lys 100 105 110	336
agc ctg ggg cgt gtg ctg tct gta ttc cat aac cgt cgc tgg gat agc Ser Leu Gly Arg Val Leu Ser Val Phe His Asn Arg Arg Trp Asp Ser 115 120 125	384
gat ttc ttg acg cta aaa ggt tta ctc gcg gaa ggc gtg ctg ggt gaa Asp Phe Leu Thr Leu Lys Gly Leu Leu Ala Glu Gly Val Leu Gly Glu 130 135 140	432
gtt gct tac ttt gag tct cat ttt gac cgc ttc cgt ccg cag gtg cgc Val Ala Tyr Phe Glu Ser His Phe Asp Arg Phe Arg Pro Gln Val Arg 145 150 155 160	480
gat cgt tgg cgt gaa cag ggc ggc cca ggc agc ggt atc tgg tac gat Asp Arg Trp Arg Glu Gln Gly Gly Pro Gly Ser Gly Ile Trp Tyr Asp 165 170 175	528
tta gca cca cat ctt ctt gat cag gcc att acg ctt ttt ggt tta ccg Leu Ala Pro His Leu Leu Asp Gln Ala Ile Thr Leu Phe Gly Leu Pro 180 185 190	576
gtc agc atg acg gta gat ttg gca cag tta cgg ccc gga gcg cag tcg Val Ser Met Thr Val Asp Leu Ala Gln Leu Arg Pro Gly Ala Gln Ser 195 200 205	624
acc gat tat ttc cac gcc atc ttg tcc tat cca cag cgg cga gtc att Thr Asp Tyr Phe His Ala Ile Leu Ser Tyr Pro Gln Arg Arg Val Ile 210 215 220	672
tta cac ggt acc atg ctg gca ggc gct gag tca gca cgg tat atc gtg Leu His Gly Thr Met Leu Ala Ala Glu Ser Ala Arg Tyr Ile Val 225 230 235 240	720
cat gga tcc cga ggc agt tat gtg aaa tat ggc ctc gat cca cag gaa His Gly Ser Arg Gly Ser Tyr Val Lys Tyr Gly Leu Asp Pro Gln Glu 245 250 255	768
gaa cgt ctg aaa aat ggc gag cgt cta ccg cag gaa gac tgg ggc tac Glu Arg Leu Lys Asn Gly Glu Arg Leu Pro Gln Glu Asp Trp Gly Tyr 260 265 270	816
gat atg cgt gat ggc gta ctt acc ccg gtg gaa ggt gag gaa cgt gtc Asp Met Arg Asp Gly Val Leu Thr Arg Val Glu Gly Glu Glu Arg Val 275 280 285	864
gaa gaa acg ctg ttg acg gtg cct ggg aat tat ccg gct tac tat ccg Glu Glu Thr Leu Leu Thr Val Pro Gly Asn Tyr Pro Ala Tyr Tyr Ala 290 295 300	912
gct att cgt gat ggc tta aat ggc gat ggt gaa aat ccg gtt ccg gca Ala Ile Arg Asp Ala Leu Asn Gly Asp Gly Glu Asn Pro Val Pro Ala 305 310 315 320	960

agc cag gca atc cag gta atg gag ttg att gag ctg ggc atc gaa tcc			1008
Ser Gln Ala Ile Gln Val Met Glu Leu Ile Glu Leu Gly Ile Glu Ser			
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Ala Val Ile Ser Ser Asp Glu Thr Lys Val Lys Ala Asp Trp Pro			
35	40	45	
Thr Val Thr Val Val Ser Glu Pro Lys His Leu Phe Asn Asp Pro Asn			
50	55	60	
Ile Asp Leu Ile Val Ile Pro Thr Pro Asn Asp Thr His Phe Pro Leu			
65	70	75	80
Ala Lys Ala Ala Leu Glu Ala Gly Lys His Val Val Val Asp Lys Pro			
85	90	95	
Phe Thr Val Thr Leu Ser Gln Ala Arg Glu Leu Asp Ala Leu Ala Lys			
100	105	110	
Ser Leu Gly Arg Val Leu Ser Val Phe His Asn Arg Arg Trp Asp Ser			
115	120	125	
Asp Phe Leu Thr Leu Lys Gly Leu Leu Ala Glu Gly Val Leu Gly Glu			
130	135	140	
Val Ala Tyr Phe Glu Ser His Phe Asp Arg Phe Arg Pro Gln Val Arg			
145	150	155	160
Asp Arg Trp Arg Glu Gln Gly Gly Pro Gly Ser Gly Ile Trp Tyr Asp			
165	170	175	
Leu Ala Pro His Leu Leu Asp Gln Ala Ile Thr Leu Phe Gly Leu Pro			
180	185	190	
Val Ser Met Thr Val Asp Leu Ala Gln Leu Arg Pro Gly Ala Gln Ser			
195	200	205	
Thr Asp Tyr Phe His Ala Ile Leu Ser Tyr Pro Gln Arg Arg Val Ile			
210	215	220	
Leu His Gly Thr Met Leu Ala Ala Glu Ser Ala Arg Tyr Ile Val			
225	230	235	240
His Gly Ser Arg Gly Ser Tyr Val Lys Tyr Gly Leu Asp Pro Gln Glu			
245	250	255	
Glu Arg Leu Lys Asn Gly Glu Arg Leu Pro Gln Glu Asp Trp Gly Tyr			
260	265	270	

Asp Met Arg Asp Gly Val Leu Thr Arg Val Glu Gly Glu Glu Arg Val
 275 : 280 285
 Glu Glu Thr Leu Leu Thr Val Pro Gly Asn Tyr Pro Ala Tyr Tyr Ala
 290 295 300
 Ala Ile Arg Asp Ala Leu Asn Gly Asp Gly Glu Asn Pro Val Pro Ala
 305 310 315 320
 Ser Gln Ala Ile Gln Val Met Glu Leu Ile Glu Leu Gly Ile Glu Ser
 325 330 335
 Ala Lys His Arg Ala Thr Leu Cys Leu Ala
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<210> 3

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<212> DNA

<213> Agrobacterium tumefaciens

<220>

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<222> (1)...(1170)

<223>

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atg gtc ggc ggc ggt cag ggc gcc ttc att ggc gcg gtg cat cgc atc	96
Met Val Gly Gly Gln Gly Ala Phe Ile Gly Ala Val His Arg Ile	
20 25 30	
gcg gcc cgg ctg gat gac cgt tac gag ctg gtg gcc gga gcg ctt tcc	144
Ala Ala Arg Leu Asp Asp Arg Tyr Glu Leu Val Ala Gly Ala Leu Ser	
35 40 45	
tcc gat ccc gcg cgt gcc gcc tcg gca aca ctg ctc ggc att gcg	192
Ser Asp Pro Ala Arg Ala Ala Ser Ala Thr Leu Leu Gly Ile Ala	
50 55 60	
ccg gag cgc tcc tat gcc tcg ttc gag gac atg gcg gcg act gag gcc	240
Pro Glu Arg Ser Tyr Ala Ser Phe Glu Asp Met Ala Ala Thr Glu Ala	
65 70 75 80	
ggc cgg gag gat ggc atc gag gca gtc gcc atc gtc acc ccc aac cat	288
Gly Arg Glu Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro Asn His	
85 90 95	
ctg cat ttt gcc cgg tcc aag gcc ttt ctc gaa gcc ggc atc cac gtc	336
Leu His Phe Ala Pro Ser Lys Ala Phe Leu Glu Ala Gly Ile His Val	
100 105 110	
atc tgc gac aag ccg gtg acc gcg acg ctg gaa gaa gcg aag gca ctg	384
Ile Cys Asp Lys Pro Val Thr Ala Thr Leu Glu Ala Lys Ala Leu	
115 120 125	
gcc ggg atc gtc aga gcc tcg gat agc ctt ttc gtg ctg acg cat aac	432

Ala Gly Ile Val Arg Ala Ser Asp Ser Leu Phe Val Leu Thr His Asn			
130	135	140	:
tac acc ggt tac gcc atg ctg cgg cag atg cgc gag atg atc got gaa			480
Tyr Thr Gly Tyr Ala Met Leu Arg Gln Met Arg Glu Met Ile Ala Glu			
145	150	155	160
ggc gcc att ggc aag ctg cgc cat gtc cag gcc gaa tat gcg cag gac			528
Gly Ala Ile Gly Lys Leu Arg His Val Gln Ala Glu Tyr Ala Gln Asp			
165	170	175	
tgg ctg acc gaa ggc gtc gaa aaa acc ggc gca aaa ggt gcg gaa tgg			576
Trp Leu Thr Glu Ala Val Glu Lys Thr Gly Ala Lys Gly Ala Glu Trp			
180	185	190	
cgc acc gac ccc agc cgc tcc ggt gcg ggc ggc atc ggc gat atc			624
Arg Thr Asp Pro Ser Arg Ser Gly Ala Gly Gly Ala Ile Gly Asp Ile			
195	200	205	
ggc act cac gcc ttc aac gct gct gcc ttt gtg acg ggt gaa atc ccc			672
Gly Thr His Ala Phe Asn Ala Ala Ala Phe Val Thr Gly Glu Ile Pro			
210	215	220	
agc agt ctt tat gcg gat ctc acg tcg ttt gtg ccg ggc cgg cag ctg			720
Ser Ser Leu Tyr Ala Asp Leu Thr Ser Phe Val Pro Gly Arg Gln Leu			
225	230	235	240
gat gac agc gcc aat att ctt ttg cgt tac gac agt ggc gcc aag ggc			768
Asp Asp Ser Ala Asn Ile Leu Leu Arg Tyr Asp Ser Gly Ala Lys Gly			
245	250	255	
atg ctc tgg gca agc cag atc gcg gtc ggc aat gaa aat gcg ctg tca			816
Met Leu Trp Ala Ser Gln Ile Ala Val Gly Asn Glu Asn Ala Leu Ser			
260	265	270	
ctc cgg gtc tat ggc gac aag ggc ggg ctt gaa tgg cac cac cgg gtg			864
Leu Arg Val Tyr Gly Asp Lys Gly Gly Leu Glu Trp His His Arg Val			
275	280	285	
ccg gac gag ctg tgg ttc acg ccc tat ggc gag cog aag cgg ctg att			912
Pro Asp Glu Leu Trp Phe Thr Pro Tyr Gly Glu Pro Lys Arg Leu Ile			
290	295	300	
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Thr Arg Asn Gly Ala Gly Ala Ala Ala Asn Arg Val Ser Arg			
305	310	315	320
gtg cca tcc ggg cac ccc gag gga tat ctc gag ggt ttt gcg acg att			1008
Val Pro Ser Gly His Pro Glu Gly Tyr Leu Glu Gly Phe Ala Thr Ile			
325	330	335	
tac cgc gaa gcc gca gac gca atc atc gca aag agg gag gga gaa aca			1056
Tyr Arg Glu Ala Ala Asp Ala Ile Ile Ala Lys Arg Glu Gly Glu Thr			
340	345	350	
gcc gcc ggg gag gtg att tac ccc ggc atg gag gac ggc ctt gcg ggt			1104
Ala Ala Gly Glu Val Ile Tyr Pro Gly Met Glu Asp Gly Leu Ala Gly			
355	360	365	
ctc gca ttc atc gat gcg gcc gtt cgc tcc agc cag acc tcg acc tgg			1152
Leu Ala Phe Ile Asp Ala Ala Val Arg Ser Ser Gln Thr Ser Thr Trp			
370	375	380	
gtc ggg atc gac atc tag			1170

Val Gly Ile Asp Ile
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<211> 389

<212> PRT

<213> Agrobacterium tumefaciens

<400> 4

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	20							25						30	
Ala	Ala	Arg	Leu	Asp	Asp	Arg	Tyr	Glu	Leu	Val	Ala	Gly	Ala	Leu	Ser
	35							40						45	
Ser	Asp	Pro	Ala	Arg	Ala	Ala	Ser	Ala	Thr	Leu	Gly	Ile	Ala		
	50							55						60	
Pro	Glu	Arg	Ser	Tyr	Ala	Ser	Phe	Glu	Asp	Met	Ala	Ala	Thr	Glu	Ala
	65							70						80	
Gly	Arg	Glu	Asp	Gly	Ile	Glu	Ala	Val	Ala	Ile	Val	Thr	Pro	Asn	His
	85							90						95	
Leu	His	Phe	Ala	Pro	Ser	Lys	Ala	Phe	Leu	Glu	Ala	Gly	Ile	His	Val
	100							105						110	
Ile	Cys	Asp	Lys	Pro	Val	Thr	Ala	Thr	Leu	Glu	Glu	Ala	Lys	Ala	Leu
	115							120						125	
Ala	Gly	Ile	Val	Arg	Ala	Ser	Asp	Ser	Leu	Phe	Val	Leu	Thr	His	Asn
	130							135						140	
Tyr	Thr	Gly	Tyr	Ala	Met	Leu	Arg	Gln	Met	Arg	Glu	Met	Ile	Ala	Glu
	145							150						160	
Gly	Ala	Ile	Gly	Lys	Leu	Arg	His	Val	Gln	Ala	Glu	Tyr	Ala	Gln	Asp
	165							170						175	
Trp	Leu	Thr	Glu	Ala	Val	Glu	Lys	Thr	Gly	Ala	Lys	Gly	Ala	Glu	Trp
	180							185						190	
Arg	Thr	Asp	Pro	Ser	Arg	Ser	Gly	Ala	Gly	Gly	Ala	Ile	Gly	Asp	Ile
	195							200						205	
Gly	Thr	His	Ala	Phe	Asn	Ala	Ala	Ala	Phe	Val	Thr	Gly	Glu	Ile	Pro
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Ser	Ser	Leu	Tyr	Ala	Asp	Leu	Thr	Ser	Phe	Val	Pro	Gly	Arg	Gln	Leu
	225							230						240	
Asp	Asp	Ser	Ala	Asn	Ile	Leu	Leu	Arg	Tyr	Asp	Ser	Gly	Ala	Lys	Gly
	245							250						255	
Met	Leu	Trp	Ala	Ser	Gln	Ile	Ala	Val	Gly	Asn	Glu	Asn	Ala	Leu	Ser
	260							265						270	
Leu	Arg	Val	Tyr	Gly	Asp	Lys	Gly	Gly	Leu	Glu	Trp	His	His	Arg	Val
	275							280						285	
Pro	Asp	Glu	Leu	Trp	Phe	Thr	Pro	Tyr	Gly	Glu	Pro	Lys	Arg	Leu	Ile
	290							295						300	

Thr Arg Asn Gly Ala Gly Ala Ala Ala Asn Arg Val Ser Arg
 305 310 315 320
 Val Pro Ser Gly His Pro Glu Gly Tyr Leu Glu Gly Phe Ala Thr Ile
 325 330 335
 Tyr Arg Glu Ala Ala Asp Ala Ile Ile Ala Lys Arg Glu Gly Glu Thr
 340 345 350
 Ala Ala Gly Glu Val Ile Tyr Pro Gly Met Glu Asp Gly Leu Ala Gly
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 370 375 380
 Val Gly Ile Asp Ile
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 <213> Agrobacterium tumefaciens

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 Leu Gly Met Val Gly Gly Ser Gly Ala Phe Ile Gly Gly Val His
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 cgc atg gca gcg cgg ctc gac aat cgc ttc gat ctc gtg gcg ggg gcc 144
 Arg Met Ala Ala Arg Leu Asp Asn Arg Phe Asp Leu Val Ala Gly Ala
 35 40 45
 ctg tcc tcg aca ccg gaa aaa tcc cta gct tcc ggg cgt gag ctg ggg 192
 Leu Ser Ser Thr Pro Glu Lys Ser Leu Ala Ser Gly Arg Glu Leu Gly
 50 55 60
 ctc gac tct gag cgt tgc tac ggc tcg ttt gaa gaa atg gcc gaa aaa 240
 Leu Asp Ser Glu Arg Cys Tyr Gly Ser Phe Glu Glu Met Ala Glu Lys
 65 70 75 80
 gaa gcg ctg cgc gag gat ggt atc gag gcg gtg gog atc gtc acc ccc 288
 Glu Ala Leu Arg Glu Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro
 85 90 95
 aac cat gtg cac tat ccc gct gca aag gcc ttc ctg gag cgc ggc atc 336
 Asn His Val His Tyr Pro Ala Ala Lys Ala Phe Leu Glu Arg Gly Ile
 100 105 110
 cat gtc atc tgc gac aag ccg ctg act tcc aat ctc gaa gac gog aaa 384
 His Val Ile Cys Asp Lys Pro Leu Thr Ser Asn Leu Glu Asp Ala Lys

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130 135 140			
cat aac tac acc ggt tat cca atg gtg cgg cat gcg cgc gag ctg gtg His Asn Tyr Thr Gly Tyr Pro Met Val Arg His Ala Arg Glu Leu Val			480
145 150 155 160			
gag gcc ggt gca ctc ggc aat atc cgt ctg gtg caa atg gaa tat ccg Glu Ala Gly Ala Leu Gly Asn Ile Arg Leu Val Gln Met Glu Tyr Pro			528
165 170 175			
cag gac tgg ctg acg gag gcg gtg gaa cag acc ggc gcg aaa cag gca Gln Asp Trp Leu Thr Glu Ala Val Glu Gln Thr Gly Ala Lys Gln Ala			576
180 185 190			
gtc tgg cgt acc gat ccg gcc caa tct ggc gtt ggc ggt tcc acc ggt Val Trp Arg Thr Asp Pro Ala Gln Ser Gly Val Gly Gly Ser Thr Gly			624
195 200 205			
gac atc ggc acc cat gcc tat aat ctc ggc tgc ttc att tcc ggt ctc Asp Ile Gly Thr His Ala Tyr Asn Leu Gly Cys Phe Ile Ser Gly Leu			672
210 215 220			
gaa gcg gat gag ctg gcg gcg gat gtg cat acc ttc gtc gaa ggc cgt Glu Ala Asp Glu Leu Ala Ala Asp Val His Thr Phe Val Glu Gly Arg			720
225 230 235 240			
cgg ctc gat gac aat gct cat gtg atg atg cgc ttc aag ccc aag ggc Arg Leu Asp Asp Asn Ala His Val Met Met Arg Phe Lys Pro Lys Gly			768
245 250 255			
ggc aag caa ccc gcc agg ggc atg ctc tgg tgc agc cag gtg gca gtc Gly Lys Gln Pro Ala Arg Gly Met Leu Trp Cys Ser Gln Val Ala Val			816
260 265 270			
ggc cat gaa aat ggg ctg aag atc cgc ctt tat ggc gac aag gcc ggt Gly His Glu Asn Gly Leu Lys Ile Arg Leu Tyr Gly Asp Lys Ala Gly			864
275 280 285			
ctc gaa tgg acg cag gcc gat ccg aat tat ctg tgg ttt acg aag ctc Leu Glu Trp Thr Gln Ala Asp Pro Asn Tyr Leu Trp Phe Thr Lys Leu			912
290 295 300			
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305 310 315 320			
gca gcc gct cgc gtt acc cgc ata ccc tcc ggc cat ccg gaa gga tat Ala Ala Ala Arg Val Thr Arg Ile Pro Ser Gly His Pro Glu Gly Tyr			1008
325 330 335			
ctg gaa gcc ttc gct acc atc tat acc gag gct gcg cat gcc att gag Leu Glu Ala Phe Ala Thr Ile Tyr Thr Glu Ala Ala His Ala Ile Glu			1056
340 345 350			
gcg cgc cgc acc ggt tcg gcg ctg gat aag gcg gtc atc tat ccg acg Ala Arg Arg Thr Gly Ser Ala Leu Asp Lys Ala Val Ile Tyr Pro Thr			1104
355 360 365			
gtg gat gac ggc gtc aaa ggt gtg gcc ttc gtc acg gcc tgc atc gag Val Asp Asp Gly Val Lys Gly Val Ala Phe Val Thr Ala Cys Ile Glu			1152

370	375	380	
tca ggc aag aag aat ggc ggc tgg gtg aag ctg taa			
Ser Gly Lys Lys Asn Gly Gly Trp Val Lys Leu			
385	390	395	1188

<210> 6
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 <213> Agrobacterium tumefaciens

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 35 40 45
 Leu Ser Ser Thr Pro Glu Lys Ser Leu Ala Ser Gly Arg Glu Leu Gly
 50 55 60
 Leu Asp Ser Glu Arg Cys Tyr Gly Ser Phe Glu Glu Met Ala Glu Lys
 65 70 75 80
 Glu Ala Leu Arg Glu Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro
 85 90 95
 Asn His Val His Tyr Pro Ala Ala Lys Ala Phe Leu Glu Arg Gly Ile
 100 105 110
 His Val Ile Cys Asp Lys Pro Leu Thr Ser Asn Leu Glu Asp Ala Lys
 115 120 125
 Lys Leu Lys Asp Val Ala Asp Ala Asp Ala Leu Phe Ile Leu Thr
 130 135 140
 His Asn Tyr Thr Gly Tyr Pro Met Val Arg His Ala Arg Glu Leu Val
 145 150 155 160
 Glu Ala Gly Ala Leu Gly Asn Ile Arg Leu Val Gln Met Glu Tyr Pro
 165 170 175
 Gln Asp Trp Leu Thr Glu Ala Val Glu Gln Thr Gly Ala Lys Gln Ala
 180 185 190
 Val Trp Arg Thr Asp Pro Ala Gln Ser Gly Val Gly Gly Ser Thr Gly
 195 200 205
 Asp Ile Gly Thr His Ala Tyr Asn Leu Gly Cys Phe Ile Ser Gly Leu
 210 215 220
 Glu Ala Asp Glu Leu Ala Ala Asp Val His Thr Phe Val Glu Gly Arg
 225 230 235 240
 Arg Leu Asp Asp Asn Ala His Val Met Met Arg Phe Lys Pro Lys Gly
 245 250 255
 Gly Lys Gln Pro Ala Arg Gly Met Leu Trp Cys Ser Gln Val Ala Val
 260 265 270
 Gly His Glu Asn Gly Leu Lys Ile Arg Leu Tyr Gly Asp Lys Ala Gly
 275 280 285

Leu Glu Trp Thr Gln Ala Asp Pro Asn Tyr Leu Trp Phe Thr Lys Leu
 290 295 300
 Gly Glu Pro Lys Gln Leu Ile Thr Arg Gly Gly Ala Gly Ala Gly Ala
 305 310 315 320
 Ala Ala Ala Arg Val Thr Arg Ile Pro Ser Gly His Pro Glu Gly Tyr
 325 330 335
 Leu Glu Ala Phe Ala Thr Ile Tyr Thr Glu Ala Ala His Ala Ile Glu
 340 345 350
 Ala Arg Arg Thr Gly Ser Ala Leu Asp Lys Ala Val Ile Tyr Pro Thr
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 <212> DNA
 <213> *Bacillus subtilis*

<220>
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 Gly Ile Leu Gly Tyr Gly Leu Ser Gly Ser Val Phe His Gly Pro Leu
 20 25 30
 ctg gat gtt ctg gat gaa tat caa atc agc aaa atc atg aca tca ccg 144
 Leu Asp Val Leu Asp Glu Tyr Gln Ile Ser Lys Ile Met Thr Ser Arg
 35 40 45
 aca gaa gaa gtg aaa ccg gat ttt cca gat gct gag gtt gta cat gag 192
 Thr Glu Glu Val Lys Arg Asp Phe Pro Asp Ala Glu Val Val His Glu
 50 55 60
 ctt gaa gaa atc aca aat gac cct gcc att gag ctt gtc att gtc acc 240
 Leu Glu Glu Ile Thr Asn Asp Pro Ala Ile Glu Leu Val Ile Val Thr
 65 70 75 80
 acc ccg agc ggc ctt cat tac gag cat act atg gca tgc ata cag gcc 288
 Thr Pro Ser Gly Leu His Tyr Glu His Thr Met Ala Cys Ile Gln Ala
 85 90 95
 gga aaa cat gtt gtg atg gaa aaa cca atg aca gca acg gcc gaa gag 336
 Gly Lys His Val Val Met Glu Lys Pro Met Thr Ala Thr Ala Glu Glu
 100 105 110

ggg gaa aca tta aaa agg gct gcc gat gaa aaa ggc gta tta tta agc Gly Glu Thr Leu Lys Arg Ala Ala Asp Glu Lys Gly Val Leu Leu Ser	384
115 120 125	
gta tat cat aac cga cgc tgg gat aac gat ttt tta acg att aaa aag Val Tyr His Asn Arg Arg Trp Asp Asn Asp Phe Leu Thr Ile Lys Lys	432
130 135 140	
ctg atc tct gag gga tcc ctt gaa gat atc aat aca tat caa gtt tcc Leu Ile Ser Glu Gly Ser Leu Glu Asp Ile Asn Thr Tyr Gln Val Ser	480
145 150 155 160	
tat aac cgc tac aga cct gaa gtt caa gcg cgg tgg cgg gaa aaa gaa Tyr Asn Arg Tyr Arg Pro Glu Val Gln Ala Arg Trp Arg Glu Lys Glu	528
165 170 175	
ggc act gcc act ggt acg ctg tat gat ctc ggc tcc cac atc ata gac Gly Thr Ala Thr Gly Thr Leu Tyr Asp Leu Gly Ser His Ile Ile Asp	576
180 185 190	
caa acc ctg cat ttg ttt ggg atg cct aaa gcc gtg act gca aac gtg Gln Thr Leu His Leu Phe Gly Met Pro Lys Ala Val Thr Ala Asn Val	624
195 200 205	
atg gcc cag cgg gaa aat gcc gaa acg gtt gac tat ttt cat tta acc Met Ala Gln Arg Glu Asn Ala Glu Thr Val Asp Tyr Phe His Leu Thr	672
210 215 220	
ctg gat tat ggc aag ctt caa gcc att cta tac gga gga tca atc gtt Leu Asp Tyr Gly Lys Leu Gln Ala Ile Leu Tyr Gly Ser Ile Val	720
225 230 235 240	
ccg gca aac gga cct cgt tat caa atc cat gga aaa gat tct acg ttt Pro Ala Asn Gly Pro Arg Tyr Gln Ile His Gly Lys Asp Ser Ser Phe	768
245 250 255	
atc aaa tat gga att gac gga cag gaa gac gca ctc aga gcg gga aga Ile Lys Tyr Ile Asp Gly Gln Glu Asp Ala Leu Arg Ala Gly Arg	816
260 265 270	
aaa cca gag gat gac agc tgg ggt gcg gat gtt ccg gag ttt tac gga Lys Pro Glu Asp Asp Ser Trp Gly Ala Asp Val Pro Glu Phe Tyr Gly	864
275 280 285	
aag ctt aca acc att cgt ggc tcc gac aaa aaa aca gaa acg att cca Lys Leu Thr Thr Ile Arg Gly Ser Asp Lys Lys Thr Glu Thr Ile Pro	912
290 295 300	
tca gta aat ggc tcc tac ctt act tat tac cgt aaa ata gcg gaa agc Ser Val Asn Gly Ser Tyr Leu Thr Tyr Arg Lys Ile Ala Glu Ser	960
305 310 315 320	
ata cga gaa ggt gct gcg ctg cca gtc act gct gag gaa ggt att aat Ile Arg Glu Gly Ala Ala Leu Pro Val Thr Ala Glu Glu Gly Ile Asn	1008
325 330 335	
gtc atc cgc atc att gaa gcc gcg atg gaa agc agt aaa gag aaa cga Val Ile Arg Ile Ile Glu Ala Ala Met Glu Ser Ser Lys Glu Lys Arg	1056
340 345 350	
acc att atg ctg gag cac taa Thr Ile Met Leu Glu His	1077
355	

<210> 8
 <211> 358
 <212> PRT
 <213> *Bacillus subtilis*

<400> 8
 Met Ile Thr Leu Leu Lys Gly Arg Arg Lys Val Asp Thr Ile Lys Val
 1 5 10 15
 Gly Ile Leu Gly Tyr Gly Leu Ser Gly Ser Val Phe His Gly Pro Leu
 20 25 30
 Leu Asp Val Leu Asp Glu Tyr Gln Ile Ser Lys Ile Met Thr Ser Arg
 35 40 45
 Thr Glu Glu Val Lys Arg Asp Phe Pro Asp Ala Glu Val Val His Glu
 50 55 60
 Leu Glu Glu Ile Thr Asn Asp Pro Ala Ile Glu Leu Val Ile Val Thr
 65 70 75 80
 Thr Pro Ser Gly Leu His Tyr Glu His Thr Met Ala Cys Ile Gln Ala
 85 90 95
 Gly Lys His Val Val Met Glu Lys Pro Met Thr Ala Thr Ala Glu Glu
 100 105 110
 Gly Glu Thr Leu Lys Arg Ala Ala Asp Glu Lys Gly Val Leu Leu Ser
 115 120 125
 Val Tyr His Asn Arg Arg Trp Asp Asn Asp Phe Leu Thr Ile Lys Lys
 130 135 140
 Leu Ile Ser Glu Gly Ser Leu Glu Asp Ile Asn Thr Tyr Gln Val Ser
 145 150 155 160
 Tyr Asn Arg Tyr Arg Pro Glu Val Gln Ala Arg Trp Arg Glu Lys Glu
 165 170 175
 Gly Thr Ala Thr Gly Thr Leu Tyr Asp Leu Gly Ser His Ile Ile Asp
 180 185 190
 Gln Thr Leu His Leu Phe Gly Met Pro Lys Ala Val Thr Ala Asn Val
 195 200 205
 Met Ala Gln Arg Glu Asn Ala Glu Thr Val Asp Tyr Phe His Leu Thr
 210 215 220
 Leu Asp Tyr Gly Lys Leu Gln Ala Ile Leu Tyr Gly Gly Ser Ile Val
 225 230 235 240
 Pro Ala Asn Gly Pro Arg Tyr Gln Ile His Gly Lys Asp Ser Ser Phe
 245 250 255
 Ile Lys Tyr Gly Ile Asp Gly Gln Glu Asp Ala Leu Arg Ala Gly Arg
 260 265 270
 Lys Pro Glu Asp Asp Ser Trp Gly Ala Asp Val Pro Glu Phe Tyr Gly
 275 280 285
 Lys Leu Thr Thr Ile Arg Gly Ser Asp Lys Lys Thr Glu Thr Ile Pro
 290 295 300
 Ser Val Asn Gly Ser Tyr Leu Thr Tyr Tyr Arg Lys Ile Ala Glu Ser
 305 310 315 320

Ile Arg Glu Gly Ala Ala Leu Pro Val Thr Ala Glu Glu Gly Ile Asn
 325 330 335
 Val Ile Arg Ile Ile Glu Ala Ala Met Glu Ser Ser Lys Glu Lys Arg
 340 345 350
 Thr Ile Met Leu Glu His
 355

<210> 9
 <211> 1170
 <212> DNA
 <213> Agrobacterium sp.

<220>
 <221> CDS
 <222> (1)..(1170)
 <223>

<400> 9						
atg tcc tcc gca cca aaa aaa ttc gac agc cgc cgt atc cgt ctc gga						48
Met Ser Ser Ala Pro Lys Lys Phe Asp Ser Arg Arg Ile Arg Leu Gly						
1 5 10 15						
atg gtc ggc ggc ggt cag ggc gcc ttt atc ggt gog gtg cac cgc ata						96
Met Val Gly Gly Gln Gly Ala Phe Ile Gly Ala Val His Arg Ile						
20 25 30						
gcg gcc cgg ctg gat gac cgt tac gag ctc gtg gcc ggc ctt tcc						144
Ala Ala Arg Leu Asp Asp Arg Tyr Glu Leu Val Ala Gly Ala Leu Ser						
35 40 45						
tcc gat ccc gcg cgt gcg gcc gct tcg gca acc ctg ctc ggc atc gcg						192
Ser Asp Pro Ala Arg Ala Ala Ser Ala Thr Leu Leu Gly Ile Ala						
50 55 60						
ccg gag cgt tcc tat gcc tca ttc gag gag atg gct gcg gca gag gcc						240
Pro Glu Arg Ser Tyr Ala Ser Phe Glu Glu Met Ala Ala Ala Glu Ala						
65 70 75 80						
ggt cga gac gac ggt atc gag gca gtc gcc atc gtg acg ccc aat cac						288
Gly Arg Asp Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro Asn His						
85 90 95						
ctc cat ttt gcg ccc tca aag gcc ttt ctc gag gcc ggt att cac gtc						336
Leu His Phe Ala Pro Ser Lys Ala Phe Leu Glu Ala Gly Ile His Val						
100 105 110						
atc tgc gac aag cct gtg acc gcg aca ctt gag gaa gca aag gcg ctg						384
Ile Cys Asp Lys Pro Val Thr Ala Thr Leu Glu Ala Lys Ala Leu						
115 120 125						
gcc gag atc gtc agg gcg tcg gac agc ctg ttt gtc ctg acg cat aat						432
Ala Glu Ile Val Arg Ala Ser Asp Ser Leu Phe Val Leu Thr His Asn						
130 135 140						
tac acc ggc tac gcc atg ctg cgg cag atg cgg cag atg gtg gct gat						480
Tyr Thr Gly Tyr Ala Met Leu Arg Gln Met Arg Gln Met Val Ala Asp						

145	150	155	160	
gga gcc att ggc aag ctg cgc cac gtt cag gcc gaa tat gcc; cag gac				528
Gly Ala Ile Gly Lys Leu Arg His Val Gln Ala Glu Tyr Ala Gln Asp				
165	170	175		
tgg ctg acc gag gcg gtt gag aag acc ggt gcg aag ggg gcg gaa tgg				576
Trp Leu Thr Glu Ala Val Glu Lys Thr Gly Ala Lys Gly Ala Glu Trp				
180	185	190		
cgc acc gat ccc agc cgc tcc ggc gcg ggc ggg gcc atc ggc gat atc				624
Arg Thr Asp Pro Ser Arg Ser Gly Ala Gly Gly Ala Ile Gly Asp Ile				
195	200	205		
ggc acc cac gcc ttc aac gct gcc gcc ttc gtt acc ggt gaa atc ccg				672
Gly Thr His Ala Phe Asn Ala Ala Ala Phe Val Thr Gly Glu Ile Pro				
210	215	220		
aag agt ctt tat gcc gac ctg acc tct ttc gtg ccg ggc cgg cag ctg				720
Lys Ser Leu Tyr Ala Asp Leu Thr Ser Phe Val Pro Gly Arg Gln Leu				
225	230	235	240	
gat gac agc gcc aat att ctt ttg cgt tac gaa agc ggc gcc aag ggc				768
Asp Asp Ser Ala Asn Ile Leu Leu Arg Tyr Glu Ser Gly Ala Lys Gly				
245	250	255		
atg ctt tgg gca agc cag atc gca gtc ggc aat gaa aac ggc ctg tcg				816
Met Leu Trp Ala Ser Gln Ile Ala Val Gly Asn Glu Asn Ala Leu Ser				
260	265	270		
ctg cgg gtc tac ggc gaa aag ggc ggg ctt gaa tgg cac cac cgc gtg				864
Leu Arg Val Tyr Gly Glu Lys Gly Leu Glu Trp His His Arg Val				
275	280	285		
ccg gat gag ctg tgg ttc acc cct tac ggc gag ccg aag ccg ctc ata				912
Pro Asp Glu Leu Trp Phe Thr Pro Tyr Gly Glu Pro Lys Arg Leu Ile				
290	295	300		
acc cgc aac ggc gca ggc gca gga gcc ggc gcg aac cgt gtc agc cgc				960
Thr Arg Asn Gly Ala Gly Ala Ala Asn Arg Val Ser Arg				
305	310	315	320	
gtg cca tcg ggg cac ccg gaa gga tac ctc gag ggt ttc gcg acg atc				1008
Val Pro Ser Gly His Pro Glu Gly Tyr Leu Glu Gly Phe Ala Thr Ile				
325	330	335		
tac cgc gaa gcc gca gat gca atc att gcc aaa agg gag gga aaa gca				1056
Tyr Arg Glu Ala Ala Asp Ala Ile Ile Ala Lys Arg Glu Gly Lys Ala				
340	345	350		
gcc gcc ggg gag gtg att tac ccc ggc atg gag gac ggc ctt gcg ggt				1104
Ala Ala Gly Glu Val Ile Tyr Pro Gly Met Glu Asp Gly Leu Ala Gly				
355	360	365		
ctc gca ttc atc gat gcc gcc gtt cgc tcc agc cag acc tcg acc tgg				1152
Leu Ala Phe Ile Asp Ala Ala Val Arg Ser Ser Gln Thr Ser Thr Trp				
370	375	380		
atc aat atc gat atc tag				1170
Ile Asn Ile Asp Ile				
385				

<210> 10
 <211> 389
 <212> PRT
 <213> Agrobacterium sp.

<400> 10
 Met Ser Ser Ala Pro Lys Lys Phe Asp Ser Arg Arg Ile Arg Leu Gly
 1 5 10 15
 Met Val Gly Gly Gly Gln Gly Ala Phe Ile Gly Ala Val His Arg Ile
 20 25 30
 Ala Ala Arg Leu Asp Asp Arg Tyr Glu Leu Val Ala Gly Ala Leu Ser
 35 40 45
 Ser Asp Pro Ala Arg Ala Ala Ser Ala Thr Leu Leu Gly Ile Ala
 50 55 60
 Pro Glu Arg Ser Tyr Ala Ser Phe Glu Glu Met Ala Ala Ala Glu Ala
 65 70 75 80
 Gly Arg Asp Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro Asn His
 85 90 95
 Leu His Phe Ala Pro Ser Lys Ala Phe Leu Glu Ala Gly Ile His Val
 100 105 110
 Ile Cys Asp Lys Pro Val Thr Ala Thr Leu Glu Glu Ala Lys Ala Leu
 115 120 125
 Ala Glu Ile Val Arg Ala Ser Asp Ser Leu Phe Val Leu Thr His Asn
 130 135 140
 Tyr Thr Gly Tyr Ala Met Leu Arg Gln Met Arg Gln Met Val Ala Asp
 145 150 155 160
 Gly Ala Ile Gly Lys Leu Arg His Val Gln Ala Glu Tyr Ala Gln Asp
 165 170 175
 Trp Leu Thr Glu Ala Val Glu Lys Thr Gly Ala Lys Gly Ala Glu Trp
 180 185 190
 Arg Thr Asp Pro Ser Arg Ser Gly Ala Gly Gly Ala Ile Gly Asp Ile
 195 200 205
 Gly Thr His Ala Phe Asn Ala Ala Ala Phe Val Thr Gly Glu Ile Pro
 210 215 220
 Lys Ser Leu Tyr Ala Asp Leu Thr Ser Phe Val Pro Gly Arg Gln Leu
 225 230 235 240
 Asp Asp Ser Ala Asn Ile Leu Leu Arg Tyr Glu Ser Gly Ala Lys Gly
 245 250 255
 Met Leu Trp Ala Ser Gln Ile Ala Val Gly Asn Glu Asn Ala Leu Ser
 260 265 270
 Leu Arg Val Tyr Gly Glu Lys Gly Leu Glu Trp His His Arg Val
 275 280 285
 Pro Asp Glu Leu Trp Phe Thr Pro Tyr Gly Glu Pro Lys Arg Leu Ile
 290 295 300
 Thr Arg Asn Gly Ala Gly Ala Gly Ala Ala Asn Arg Val Ser Arg
 305 310 315 320
 Val Pro Ser Gly His Pro Glu Gly Tyr Leu Glu Gly Phe Ala Thr Ile
 325 330 335

Tyr Arg Glu Ala Ala Asp Ala Ile Ile Ala Lys Arg Glu Gly Lys Ala
 340 345 350
 Ala Ala Gly Glu Val Ile Tyr Pro Gly Met Glu Asp Gly Leu Ala Gly
 355 360 365
 Leu Ala Phe Ile Asp Ala Ala Val Arg Ser Ser Gln Thr Ser Thr Trp
 370 375 380
 Ile Asn Ile Asp Ile
 385

<210> 11
 <211> 1188
 <212> DNA
 <213> Agrobacterium sp.

<220>
 <221> CDS
 <222> (1)..(1188)
 <223>

<400> 11		
atg gct att gaa gga aag aca acc gac aag gcg aac aag cgg att cgc		48
Met Ala Ile Glu Gly Lys Thr Thr Asp Lys Ala Asn Lys Arg Ile Arg		
1 5 10 15		
ctc ggc atg gtg ggc ggt ggt tct ggt gcc ttt atc ggt ggt gtt cac		96
Leu Gly Met Val Gly Gly Ser Gly Ala Phe Ile Gly Gly Val His		
20 25 30		
cgc atg gcg gcg cgg ctc gac aat cgt ttc gat ctc gtg gca ggg gcg		144
Arg Met Ala Ala Arg Leu Asp Asn Arg Phe Asp Leu Val Ala Gly Ala		
35 40 45		
ctg tct tgc acc ccc gaa aaa tcc ctc gcc tcc ggc cgt gaa ctg ggg		192
Leu Ser Ser Thr Pro Glu Lys Ser Leu Ala Ser Gly Arg Glu Leu Gly		
50 55 60		
ctc gat ccc gag cgt tgc tac ggc tcc gag gag atg gcc gaa aag		240
Leu Asp Pro Glu Arg Cys Tyr Gly Ser Phe Glu Glu Met Ala Glu Lys		
65 70 75 80		
gag gcg cta ccc gag gat ggc ata gag gcg gtc ggc atc acg ccc		288
Glu Ala Leu Arg Glu Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro		
85 90 95		
aac cac gtg cat tat ccg gcg aag gcg ttt ctg gag cgt ggc atc		336
Asn His Val His Tyr Pro Ala Ala Lys Ala Phe Leu Glu Arg Gly Ile		
100 105 110		
cat gtc atc tgc gac aag ccg ctg acc tcc aat ctg gaa gac gcg aag		384
His Val Ile Cys Asp Lys Pro Leu Thr Ser Asn Leu Glu Asp Ala Lys		
115 120 125		
aag ctg aag gac gtc gcc gac aag gcc gat gcg ctg ttc atc ctg acg		432
Lys Leu Lys Asp Val Ala Asp Lys Ala Asp Ala Leu Phe Ile Leu Thr		
130 135 140		

cat aat tac acc ggc tat ccg atg gtg cgg cat gca cgg gaa ctg gtg His Asn Tyr Thr Gly Tyr Pro Met Val Arg His Ala Arg Glu Leu Val 145 150 155 160	480
gaa tcg ggc gct ctc ggc acg atc cgt ctg gtg cag atg gag tat ccg Glu Ser Gly Ala Leu Gly Thr Ile Arg Leu Val Gln Met Glu Tyr Pro 165 170 175	528
cag gac tgg ctg gcg gaa ccc atc gag cag acg ggc gcc aaa cag gct Gln Asp Trp Leu Ala Glu Pro Ile Glu Gln Thr Gly Ala Lys Gln Ala 180 185 190	576
gtc tgg cgc acc gac ccg gcc caa tcc ggt gcg ggt ggt tcc aca ggc Val Trp Arg Thr Asp Pro Ala Gln Ser Gly Ala Gly Gly Ser Thr Gly 195 200 205	624
gat atc ggc acg cat gcc tat aat ctc ggc tgc ttc att tcc ggt ctg Asp Ile Gly Thr His Ala Tyr Asn Leu Gly Cys Phe Ile Ser Gly Leu 210 215 220	672
gaa gtc gac gaa ctg gcg gca gat gtg cat acc ttt gtc gaa ggc cgc Glu Val Asp Glu Leu Ala Ala Asp Val His Thr Phe Val Glu Gly Arg 225 230 235 240	720
cgg ctg gac gac aat gcg cat gtg atg ctg cgt ttc aag ccg aag ggt Arg Leu Asp Asp Asn Ala His Val Met Leu Arg Phe Lys Pro Lys Gly 245 250 255	768
ggc aag cag ccg gca aag ggg ctg ctc tgg tgc acg cag gtt gcg gtc Gly Lys Gln Pro Ala Lys Gly Leu Leu Trp Cys Ser Gln Val Ala Val 260 265 270	816
ggc cac gaa aac ggc ctg aaa gtt cgt gtg tat ggt gac aag gcc ggc Gly His Glu Asn Gly Leu Lys Val Arg Val Tyr Gly Asp Lys Ala Gly 275 280 285	864
atc gaa tgg acg cag gcc gac ccg aac tat ctc tgg ttc acg aag ctt Ile Glu Trp Thr Gln Ala Asp Pro Asn Tyr Leu Trp Phe Thr Lys Leu 290 295 300	912
ggc gag ctg aag cag ttg atc acc cgc ggc ggt gcc ggg gca ggg gct Gly Glu Leu Lys Gln Leu Ile Thr Arg Gly Gly Ala Gly Ala Gly Ala 305 310 315 320	960
gcc gca gca cgc gtc acc cgc atc cct tcc ggc cac ccg gaa ggt tat Ala Ala Ala Arg Val Thr Arg Ile Pro Ser Gly His Pro Glu Gly Tyr 325 330 335	1008
ctc gaa gcc ttc gca acg atc tat acc gag gcg gcg cat gcc atc gaa Leu Glu Ala Phe Ala Thr Ile Tyr Thr Glu Ala Ala His Ala Ile Glu 340 345 350	1056
gcc cgc cgc acc ggc tcg gtg ctc gac aag gcc gtg att tac ccg acc Ala Arg Arg Thr Gly Ser Val Leu Asp Lys Ala Val Ile Tyr Pro Thr 355 360 365	1104
gtc gat gat ggc gta aag ggt gtc gcc ttt gtt acg gcc tgc atc gag Val Asp Asp Gly Val Lys Gly Val Ala Phe Val Thr Ala Cys Ile Glu 370 375 380	1152
tcc ggc aag aac aac ggt gtc tgg gtg aag ctg taa Ser Gly Lys Lys Asn Gly Val Trp Val Lys Leu 385 390 395	1188

<210> 12
 <211> 395
 <212> PRT
 <213> Agrobacterium sp.

<400> 12
 Met Ala Ile Glu Gly Lys Thr Thr Asp Lys Ala Asn Lys Arg Ile Arg
 1 5 10 15
 Leu Gly Met Val Gly Gly Ser Gly Ala Phe Ile Gly Gly Val His
 20 25 30
 Arg Met Ala Ala Arg Leu Asp Asn Arg Phe Asp Leu Val Ala Gly Ala
 35 40 45
 Leu Ser Ser Thr Pro Glu Lys Ser Leu Ala Ser Gly Arg Glu Leu Gly
 50 55 60
 Leu Asp Pro Glu Arg Cys Tyr Gly Ser Phe Glu Glu Met Ala Glu Lys
 65 70 75 80
 Glu Ala Leu Arg Glu Asp Gly Ile Glu Ala Val Ala Ile Val Thr Pro
 85 90 95
 Asn His Val His Tyr Pro Ala Ala Lys Ala Phe Leu Glu Arg Gly Ile
 100 105 110
 His Val Ile Cys Asp Lys Pro Leu Thr Ser Asn Leu Glu Asp Ala Lys
 115 120 125
 Lys Leu Lys Asp Val Ala Asp Lys Ala Asp Ala Leu Phe Ile Leu Thr
 130 135 140
 His Asn Tyr Thr Gly Tyr Pro Met Val Arg His Ala Arg Glu Leu Val
 145 150 155 160
 Glu Ser Gly Ala Leu Gly Thr Ile Arg Leu Val Gln Met Glu Tyr Pro
 165 170 175
 Gln Asp Trp Leu Ala Glu Pro Ile Glu Gln Thr Gly Ala Lys Gln Ala
 180 185 190
 Val Trp Arg Thr Asp Pro Ala Gln Ser Gly Ala Gly Ser Thr Gly
 195 200 205
 Asp Ile Gly Thr His Ala Tyr Asn Leu Gly Cys Phe Ile Ser Gly Leu
 210 215 220
 Glu Val Asp Glu Leu Ala Ala Asp Val His Thr Phe Val Glu Gly Arg
 225 230 235 240
 Arg Leu Asp Asp Asn Ala His Val Met Leu Arg Phe Lys Pro Lys Gly
 245 250 255
 Gly Lys Gln Pro Ala Lys Gly Leu Leu Trp Cys Ser Gln Val Ala Val
 260 265 270
 Gly His Glu Asn Gly Leu Lys Val Arg Val Tyr Gly Asp Lys Ala Gly
 275 280 285
 Ile Glu Trp Thr Gln Ala Asp Pro Asn Tyr Leu Trp Phe Thr Lys Leu
 290 295 300
 Gly Glu Leu Lys Gln Leu Ile Thr Arg Gly Gly Ala Gly Ala Gly Ala
 305 310 315 320

Ala Ala Ala Arg Val Thr Arg Ile Pro Ser Gly His Pro Glu Gly Tyr
 325 330 335
 Leu Glu Ala Phe Ala Thr Ile Tyr Thr Glu Ala Ala His Ala Ile Glu
 340 345 350
 Ala Arg Arg Thr Gly Ser Val Leu Asp Lys Ala Val Ile Tyr Pro Thr
 355 360 365
 Val Asp Asp Gly Val Lys Gly Val Ala Phe Val Thr Ala Cys Ile Glu
 370 375 380
 Ser Gly Lys Lys Asn Gly Val Trp Val Lys Leu
 385 390 395

<210>	13	
<211>	1059	
<212>	DNA	
<213>	Xanthomonas campestris pv. campestris	
<220>		
<221>	CDS	
<222>	(1)..(1059)	
<223>		
<400>	13	
atg cct aaa cca ttc aat ctg gcc gtc gtc ggc tat ggc tat gtt ggc		48
Met Pro Lys Pro Phe Asn Leu Ala Val Val Gly Tyr Gly Tyr Val Gly		
1 5 10 15		
cgc acc ttc cac gca ccg ctg atc gcc agc acg ccc ggc ctg cag ttg		96
Arg Thr Phe His Ala Pro Leu Ile Ala Ser Thr Pro Gly Leu Gln Leu		
20 25 30		
cac agc gtg gtg tgc tcc aag ccg cag ccg cag gcg gac ttc cgc		144
His Ser Val Val Ser Ser Lys Pro Gln Gln Pro Gln Ala Asp Phe Arg		
35 40 45		
gag gtg cgc gtg ctg ccc gac ctg gag gct gca ctg gcc gac ccg gcg		192
Glu Val Arg Val Leu Pro Asp Leu Glu Ala Ala Leu Ala Asp Pro Ala		
50 55 60		
ctg gat gcg gtg gtc atc gcc acg ccc aac cag acc cat gcg ccc atg		240
Leu Asp Ala Val Val Ile Ala Thr Pro Asn Gln Thr His Ala Pro Met		
65 70 75 80		
gcg ctg cag gca ctg gcg gcc ggc aag cac gtg ctg gtg gat aaa ccc		288
Ala Leu Gln Ala Leu Ala Ala Gly Lys His Val Leu Val Asp Lys Pro		
85 90 95		
tcc gcc ctg gat gcc gca cag gct cgc acc gtg gtg gac gcc gcc gca		336
Phe Ala Leu Asp Ala Ala Gln Ala Arg Thr Val Val Asp Ala Ala Ala		
100 105 110		
gag gcc ggc aag atc gtc agc gtg ttc cag aac cgc cgt tgg gat gcg		384
Glu Ala Gly Lys Ile Val Ser Val Phe Gln Asn Arg Arg Trp Asp Ala		
115 120 125		
gac ttc ctc acc gtg cgg cgc ttg atc gaa gac ggc caa ctg ggc gag		432

Asp Phe Leu Thr Val Arg Arg Leu Ile Glu Asp Gly Gln Leu Gly Glu			
130	135	140	
gtg gtg gag ttc cat tcg cac ttc gac cgg tat cgc ccg cag gtg cgc			480
Val Val Glu Phe His Ser His Phe Asp Arg Tyr Arg Pro Gln Val Arg			
145	150	155	160
gac cgc tgg cgc gaa agc gat atc ccc ggc gcc ggg ctg tgg tac gac			528
Asp Arg Trp Arg Glu Ser Asp Ile Pro Gln Ala Gly Leu Trp Tyr Asp			
165	170	175	
ctg ggg ccg cat ctg ctg gac cag gcg ttg cag ttg ttc ggc atg ccg			576
Leu Gly Pro His Leu Leu Asp Gln Ala Leu Gln Leu Phe Gly Met Pro			
180	185	190	
cag gcg atc agc gca gac ctg cag cgc cag ccg acc cag gcg cgc agc			624
Gln Ala Ile Ser Ala Asp Leu Gln Arg Gln Arg Thr Gln Ala Arg Ser			
195	200	205	
gac gat tac ttc aac gtc gtg ctg cgc tat ccc cgc ttg cgg gtg atc			672
Asp Asp Tyr Phe Asn Val Val Leu Arg Tyr Pro Arg Leu Arg Val Ile			
210	215	220	
ctg cac gcc ggc tcg ctg gtg gcc gac ggc agc ctg cgc ttc gcc gtg			720
Leu His Ala Gly Ser Leu Val Ala Asp Gln Ser Leu Arg Phe Ala Val			
225	230	235	240
cac ggc acg cgc ggc agc tat ctc aag cat ggc gcc gat acg cag gaa			768
His Gly Thr Arg Gly Ser Tyr Leu Lys His Gly Ala Asp Thr Gln Glu			
245	250	255	
gac cag ttg cgt gcc ggc cgc cgg ccc ggc acc gcc ggc ttg ggc atg			816
Asp Gln Leu Arg Ala Gly Arg Arg Pro Gln Thr Ala Gly Trp Gly Met			
260	265	270	
gac cca ttg ccc ggc acg ctc acc ccg gtg gac gac gaa ggc cgt gtg			864
Asp Pro Leu Pro Gln Thr Leu Thr Arg Val Asp Asp Glu Gly Arg Val			
275	280	285	
cac acg cat cag ccc gat ggc gta ccc ggc gac tac cgc cat tgc tat			912
His Thr His Gln Pro Asp Gln Val Pro Gln Asp Tyr Arg His Cys Tyr			
290	295	300	
gcg gcc ttc cgc gac gca atg gcc ggc acc gca ccg cca ccg gtc agt			960
Ala Ala Phe Arg Asp Ala Met Ala Gly Thr Ala Pro Pro Pro Val Ser			
305	310	315	320
gct gcc gac gcg gtg cgg ctg atg gag ctg ctg gag ctg gcg caa ccg			1008
Ala Ala Asp Ala Val Arg Leu Met Glu Leu Leu Glu Leu Ala Gln Arg			
325	330	335	
ggt gct gcg ctg ggc cag gtg ctc tgg ctg gaa ggc aac agc agc gac			1056
Gly Ala Ala Leu Gly Gln Val Leu Trp Leu Glu Gly Asn Ser Ser Asp			
340	345	350	
tga			1059

<210> 14

<211> 352

<212> PRT

<213> Xanthomonas campestris pv. campestris

<400> 14

Met Pro Lys Pro Phe Asn Leu Ala Val Val Gly Tyr Gly Tyr Val Gly
 1 5 10 15
 Arg Thr Phe His Ala Pro Leu Ile Ala Ser Thr Pro Gly Leu Gln Leu
 20 25 30
 His Ser Val Val Ser Ser Lys Pro Gln Gln Pro Gln Ala Asp Phe Arg
 35 40 45
 Glu Val Arg Val Leu Pro Asp Leu Glu Ala Ala Leu Ala Asp Pro Ala
 50 55 60
 Leu Asp Ala Val Val Ile Ala Thr Pro Asn Gln Thr His Ala Pro Met
 65 70 75 80
 Ala Leu Gln Ala Leu Ala Ala Gly Lys His Val Leu Val Asp Lys Pro
 85 90 95
 Phe Ala Leu Asp Ala Ala Gln Ala Arg Thr Val Val Asp Ala Ala Ala
 100 105 110
 Glu Ala Gly Lys Ile Val Ser Val Phe Gln Asn Arg Arg Trp Asp Ala
 115 120 125
 Asp Phe Leu Thr Val Arg Arg Leu Ile Glu Asp Gly Gln Leu Gly Glu
 130 135 140
 Val Val Glu Phe His Ser His Phe Asp Arg Tyr Arg Pro Gln Val Arg
 145 150 155 160
 Asp Arg Trp Arg Glu Ser Asp Ile Pro Gly Ala Gly Leu Trp Tyr Asp
 165 170 175
 Leu Gly Pro His Leu Leu Asp Gln Ala Leu Gln Leu Phe Gly Met Pro
 180 185 190
 Gln Ala Ile Ser Ala Asp Leu Gln Arg Gln Arg Thr Gln Ala Arg Ser
 195 200 205
 Asp Asp Tyr Phe Asn Val Val Leu Arg Tyr Pro Arg Leu Arg Val Ile
 210 215 220
 Leu His Ala Gly Ser Leu Val Ala Asp Gly Ser Leu Arg Phe Ala Val
 225 230 235 240
 His Gly Thr Arg Gly Ser Tyr Leu Lys His Gly Ala Asp Thr Gln Glu
 245 250 255
 Asp Gln Leu Arg Ala Gly Arg Arg Pro Gly Thr Ala Gly Trp Gly Met
 260 265 270
 Asp Pro Leu Pro Gly Thr Leu Thr Arg Val Asp Asp Glu Gly Arg Val
 275 280 285
 His Thr His Gln Pro Asp Gly Val Pro Gly Asp Tyr Arg His Cys Tyr
 290 295 300
 Ala Ala Phe Arg Asp Ala Met Ala Gly Thr Ala Pro Pro Pro Val Ser
 305 310 315 320
 Ala Ala Asp Ala Val Arg Leu Met Glu Leu Leu Glu Leu Ala Gln Arg
 325 330 335
 Gly Ala Ala Leu Gly Gln Val Leu Trp Leu Glu Gly Asn Ser Ser Asp
 340 345 350

<210> 15
<211> 34
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 15
cattcaagct taatgagagg caatgacatg agcg

34

<210> 16
<211> 31
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 16
tcggaattt tcatgcaagg cacaaagtgc c

31

<210> 17
<211> 32
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 17
ggcggatcct ttgaaaggga tagtcatgtc ct

32

<210> 18
<211> 29
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 18
atttggaaagct tcgattggct gcgacctag

29

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> primer

<400> 19
 ttgggatcct ttcagggaa atattatggc

30

<210> 20
 <211> 26
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 <213> Artificial

<220>
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<400> 20
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26

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34

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35

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39

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Met Thr Lys Arg Lys Leu Arg Ile Gly Leu Ile Gly Ser Gly Phe Met		
1 5 10 15		
ggg cgc acc cac gcc ttt ggc tat tca acc gcg tcc cgt gtg ttt gat	96	
Gly Arg Thr His Ala Phe Gly Tyr Ser Thr Ala Ser Arg Val Phe Asp		
20 25 30		
ctt ccg ttt cag ccg gag ctg acg tgc ctg gct gat att tcc gat gaa	144	
Leu Pro Phe Gln Pro Glu Leu Thr Cys Leu Ala Asp Ile Ser Asp Glu		
35 40 45		
gct gca gcg aag gcg gcg gat gct ctg gga ttt gcc cgt tcc acc agt	192	
Ala Ala Ala Lys Ala Ala Asp Ala Leu Gly Phe Ala Arg Ser Thr Ser		
50 55 60		
gac tgg cgt acg ctc gtc aac gat cct gaa att gat gtg gtg aat atc	240	
Asp Trp Arg Thr Leu Val Asn Asp Pro Glu Ile Asp Val Val Asn Ile		
65 70 75 80		
acg gcg cct aat gcc ttt cat aaa gaa atg gcg tta gca gcg att gct	288	
Thr Ala Pro Asn Ala Phe His Lys Glu Met Ala Leu Ala Ala Ile Ala		
85 90 95		
gcg ggc aag cat gtc tat tgt gaa aag ccc ctt gcg cca ctt gca gcc	336	
Ala Gly Lys His Val Tyr Cys Glu Lys Pro Leu Ala Pro Leu Ala Ala		
100 105 110		
gat gct cgc gaa atg gca gaa gcg gct gag gca aag ggc gta aaa aca	384	
Asp Ala Arg Glu Met Ala Glu Ala Ala Glu Ala Lys Gly Val Lys Thr		
115 120 125		
cag gtt ggc ttc aac tac ctg tgc aac ccc atg ctg gca ctg gcc cga	432	
Gln Val Gly Phe Asn Tyr Leu Cys Asn Pro Met Leu Ala Leu Ala Arg		
130 135 140		
gat atg att gca gca ggg gag ctg ggg gaa atc aga ggg tac cgt ggc	480	
Asp Met Ile Ala Ala Gly Glu Leu Gly Glu Ile Arg Gly Tyr Arg Gly		
145 150 155 160		
ctg cat gcg gaa gat tat atg gcg gac gcc tcg tct ccc ttt acg ttc	528	
Leu His Ala Glu Asp Tyr Met Ala Asp Ala Ser Ser Pro Phe Thr Phe		
165 170 175		
cgt ctt gac cca gcg gga ggc ggc gca ctt gct gat att ggg agt cac	576	
Arg Leu Asp Pro Ala Gly Gly Ala Leu Ala Asp Ile Gly Ser His		
180 185 190		

gcc ctt gca acg gct gaa ttt ctt atg ggg cct gcc gca ggc gct atc Ala Leu Ala Thr Ala Glu Phe Leu Met Gly Pro Ala Ala Gly Ala Ile 195 200 205	624
acg cag gtg atg ggg gat tgt gtg acg gtc atc aag acg cgg ccg gat Thr Gln Val Met Gly Asp Cys Val Thr Val Ile Lys Thr Arg Pro Asp 210 215 220	672
ggt aag ggg gga acg cgg gct gta gaa gtg gac gat att ggc cgc gcg Gly Lys Gly Gly Thr Arg Ala Val Glu Val Asp Asp Ile Gly Arg Ala 225 230 235 240	720
ctt ctg cgc ttt gag aat ggg gcg acg gga tcg gtt gag gga aac tgg Leu Leu Arg Phe Glu Asn Gly Ala Thr Gly Ser Val Glu Gly Asn Trp 245 250 255	768
att gct acc ggc cgc acc atg cag cat gac ttt gag gta tac ggc aca Ile Ala Thr Gly Arg Thr Met Gln His Asp Phe Glu Val Tyr Gly Thr 260 265 270	816
aaa ggt gca ctt gcc ttt act cag caa cga ttt aac gag ttg cat ttc Lys Gly Ala Leu Ala Phe Thr Gln Gln Arg Phe Asn Glu Leu His Phe 275 280 285	864
ttc tca agc acc gat gca cgc ggc cgc aaa ggg ttc cgg cgt att gaa Phe Ser Ser Thr Asp Ala Arg Gly Arg Lys Gly Phe Arg Arg Ile Glu 290 295 300	912
gcg gga cca gag cat gcg ccc tat ggc ctg ttc tgc gtg gca ccc ggg Ala Gly Pro Glu His Ala Pro Tyr Gly Leu Phe Cys Val Ala Pro Gly 305 310 315 320	960
cac cag ctg ggt ttt aat gac ctc aag gcg ata gaa gtt gca cgg tat His Gln Leu Gly Phe Asn Asp Leu Lys Ala Ile Glu Val Ala Arg Tyr 325 330 335	1008
ctg gag gcg ctg gct ggc cat cac ccc gaa ccc ttc aat ttc cgg gcg Leu Glu Ala Leu Ala Gly His His Pro Glu Pro Phe Asn Phe Arg Ala 340 345 350	1056
ggt ctg cgt atc cag aca ctg gtg gaa act att cac gct tca agc aag Gly Leu Arg Ile Gln Thr Leu Val Glu Thr Ile His Ala Ser Ser Lys 355 360 365	1104
tcg gct gcc tgg cgg gat gtg cgg acg gac aaa gtg aag ctt cag gcg Ser Ala Ala Trp Arg Asp Val Pro Thr Asp Lys Val Lys Leu Gln Ala 370 375 380	1152
aaa tcc cga cag cat gag aag gca taa Lys Ser Arg Gln His Glu Lys Ala 385 390	1179

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 <213> Acetobacter sp.

<400> 28
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Leu Pro Phe Gln Pro Glu Leu Thr Cys Leu Ala Asp Ile Ser Asp Glu			
35	40	45	
Ala Ala Ala Lys Ala Ala Asp Ala Leu Gly Phe Ala Arg Ser Thr Ser			
50	55	60	
Asp Trp Arg Thr Leu Val Asn Asp Pro Glu Ile Asp Val Val Asn Ile			
65	70	75	80
Thr Ala Pro Asn Ala Phe His Lys Glu Met Ala Leu Ala Ala Ile Ala			
85	90	95	
Ala Gly Lys His Val Tyr Cys Glu Lys Pro Leu Ala Pro Leu Ala Ala			
100	105	110	
Asp Ala Arg Glu Met Ala Glu Ala Ala Glu Ala Lys Gly Val Lys Thr			
115	120	125	
Gln Val Gly Phe Asn Tyr Leu Cys Asn Pro Met Leu Ala Leu Ala Arg			
130	135	140	
Asp Met Ile Ala Ala Gly Glu Leu Gly Glu Ile Arg Gly Tyr Arg Gly			
145	150	155	160
Leu His Ala Glu Asp Tyr Met Ala Asp Ala Ser Ser Pro Phe Thr Phe			
165	170	175	
Arg Leu Asp Pro Ala Gly Gly Ala Leu Ala Asp Ile Gly Ser His			
180	185	190	
Ala Leu Ala Thr Ala Glu Phe Leu Met Gly Pro Ala Ala Gly Ala Ile			
195	200	205	
Thr Gln Val Met Gly Asp Cys Val Thr Val Ile Lys Thr Arg Pro Asp			
210	215	220	
Gly Lys Gly Gly Thr Arg Ala Val Glu Val Asp Asp Ile Gly Arg Ala			
225	230	235	240
Leu Leu Arg Phe Glu Asn Gly Ala Thr Gly Ser Val Glu Gly Asn Trp			
245	250	255	
Ile Ala Thr Gly Arg Thr Met Gln His Asp Phe Glu Val Tyr Gly Thr			
260	265	270	
Lys Gly Ala Leu Ala Phe Thr Gln Gln Arg Phe Asn Glu Leu His Phe			
275	280	285	
Phe Ser Ser Thr Asp Ala Arg Gly Arg Lys Gly Phe Arg Arg Ile Glu			
290	295	300	
Ala Gly Pro Glu His Ala Pro Tyr Gly Leu Phe Cys Val Ala Pro Gly			
305	310	315	320
His Gln Leu Gly Phe Asn Asp Leu Lys Ala Ile Glu Val Ala Arg Tyr			
325	330	335	
Leu Glu Ala Leu Ala Gly His His Pro Glu Pro Phe Asn Phe Arg Ala			
340	345	350	
Gly Leu Arg Ile Gln Thr Leu Val Glu Thr Ile His Ala Ser Ser Lys			
355	360	365	
Ser Ala Ala Trp Arg Asp Val Pro Thr Asp Lys Val Lys Leu Gln Ala			
370	375	380	
Lys Ser Arg Gln His Glu Lys Ala			

385 390

<210> 29
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 <212> DNA
 <213> Artificial

<220>
 <223> primer

<220>
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 <222> (9), (15)
 <223> n=a, t, g or c

<220>
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 <222> (18), (27)
 <223> n=inosine

<400> 29
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32

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 <223> n=a, t, g or c

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 <222> (18), (24)
 <223> n=inosine

<400> 30
 ggyttagg gycgnacnca ygcnttyggy ta

32

<210> 31
<211> 26
<212> DNA
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<220>
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<400> 31
ggyttrtcrm mgayracrtg rstrcc

26

<210> 32
<211> 19
<212> DNA
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<220>
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19

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gctcgtcaac gatcctgaaa ttgat

25

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ttcgctgcag cttcatcgga aatat

25

<210> 35

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<213> Artificial

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<210> 36

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<212> DNA

<213> Artificial

<220>

<223> primer

<400> 36

gctggatccc gcccttattt gataata

26

<210> 37

<211> 31

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 37

tatgaattcg ttatgccttc tcgtgtgc g

31